Shict:

```
>SD|P47901|V1BR HUMAN VASOPRESSIN V1B RECEPTOR (AVPR V1B) (VASOPRESSIN V3
            RECEPTOR) (AVPR V3) (ANTIDIURETIC HORMONE RECEPTOR 1B).
            lenath = 424
 Score = 316 (111.2 bits), Expect = 3.7e-41, Sum P(2) = 3.7e-41
Identities = 70/194 (36%), Positives = 115/194 (59%)
          56 I WVI EVETIVGNSVVLESTWRR-KKKSRMTFEVTQLAITDSFTGLVNILTDINWRFTGDF 114
Query:
                                                        L +L + W T F
                      GN VL + + +K+SRM FV LA+TD
         41 LATVLVLATGGNLAVLLTLGQLGRKRSRMHLFVLHLALTDLAVALFQVLPQLLWDITYRF 100
Sbict:
         115 TAPDLVCRVVRYLQVVLLYASTYVLVSLSIDRYHAIVYPMKFLQGEKQARVLIVIA-WSL 173
Query:
               PDL+CR V+YLQV+ ++ASTY+L+++++DRY A+ +P++ LQ Q+ L++ A W L
         101 QGPDLLCRAVKYLQVLSMFASTYMLLAMTLDRYLAVCHPLRSLQQPGQSTYLLIAAPWLL 160
Sbict:
         174 SFLFSIPTLIIFGKRTL--SNGEVQCWALWPDDSY-WTP--YMTIVAFLVYFIPLTIISI 228
Query:
             + +FS+P + IF R + +G + CWA D + W P Y+T
                                                             ++ +P+T+++
         161 AAIFSLPOVFIFSLREVIQGSGVLDCWA---DFGFPWGPRAYLTWTTLAIFVLPVTMLTA 217
Sbict:
         229 MYGIVIRTIW--IKSKT 243
Query:
              Y ++ I +K KT
         218 CYSLICHFICKNIKVKT 234
Sbict:
 Score = 131 (46.1 bits), Expect = 3.7e-41. Sum P(2) = 3.7e-41
 Identities = 33/80 (41%), Positives = 47/80 (58%)
         258 SSYNRGLISKAKIKAIKYSIIIILAFICCWSPYF---LFDILDNFNLLPDTQERFYASVI 314
Query:
                    IS+AKI+ +K + +I+LA+I CW+P+F ++ + D N PD
                                                                   A I
         267 SSINT-ISRAKIRTVKMTFVIVLAYIACWAPFFSVQMWSVWDK-NA-PDEDSTNVAFTI 322
Sbict:
         315 IONLPALNSAINPLIYCVFSSSI 337
Query:
                L LNS NP IY F+S +
```

323 SMLLGNLNSCCNPWIYMGFNSHL 345

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>sp|P31388|5H6 RAT 5-HYDROXYTRYPTAMINE 6 RECEPTOR (5-HT-6) (SEROTONIN RECEPTOR)
           (ST-B17).
           Length = 436
 Score = 224 (78.9 bits), Expect = 6.7e-17, P = 6.7e-17
 Identities = 84/309 (27%), Positives = 144/309 (46%)
          3 PGEA--LLAGLLYMVLAVALLSNALVLLCCAYSAELRTRASGVLLVNLSLGHLLLAALDM 60
Query:
            PG + + A L V+++ A ++ L++L C A LR S LV+L
Sbict:
         23 PGGSGWVAAALCVVIVLTAAANSLLIVLICTQPA-LRN-TSNFFLVSLFTSDLMVGLVVM 80
         61 PETLLGYMRGRTPSAPGACOVIGELDTFLASNAALSVAALSADOWLAVGEPLRYAGRIR- 119
Query:
            P +L + GR AGC + D
                                         S + I ++ +S D++I + PIRY R+
Sbict:
         81 PPAMLNALYGRWVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLILSPLRYKLRMTA 140
        120 PRYAGLLIGCAWGOSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAA---FTATL 176
Query:
                 L+LG AW SLA AL S+L
                                           +
                                                     PP+RAF
Sbict:
        141 PRALALILG-AW--SLA----ALA-SFLPLLLGWHELGKARTPAPGQCRLLASLPFVLVA 192
        177 HAVGEVLPLAVI CLTSI OVHRVARRHCORMDTVT------MKALALLADLHPSVR---- 225
Query:
              V F LP +C T ++ AR+ ++ ++T
                                                    ++ L +
Sbict:
        193 SGVTFFLPSGAICFTYCRILLAARKQAVQVASLTTGTAGQALETLQVPRTPRPGMESADS 252
        226 ORCLIQOKRRRHRATRKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYS 285
Querv:
            +R + R+ +A+ +GI + F + + P+ + +A+ V
                                                           + +l+ | Y
Shict:
        253 RRLATKHSRKALKASLTLGILLGMFFVTWLPFFVANIAQAVCDCISPGLFDVLT-WLGYC 311
        286 KAVADPFTYSLLRRPFRQVL 305
Query:
             + +P Y L R F++ L
Sbjct:
        312 NSTMNPIIYPLFMRDFKRAL 331
```

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>sp|P56479|GALR MOUSE GALANIN RECEPTOR TYPE 1 (GAL1-R) (GALR1).
           Length = 348
 Score = 269 (94.7 bits), Expect = 7.9e-24, P = 7.9e-24
 Identities = 82/289 (28%), Positives = 136/289 (47%)
Query:
         49 VGFVGNLCVIGILLHNAWKGKP-SMIHSLILNLSLADLSLLLFSAPIRATAYSKSVWDLG 107
            +G +GN VI +L + GKP S + ILNLS+ADL+ LLF P +AT Y+
Shict:
         46 MGVI GNSI VITVI ARSK-PGKPRSTTNI FII NI SIADI AVI I FCI PFOATVYAI PTWVI G. 104
         108 WEVCKSSDWFTHTCMAAKSLTIVVVA--KVCFMYASDPÄKOVSTHNYTTWSVI VATWTVA 165
Query:
             F+CK +F M
                               + V IW++
         105 AFICKFIHYFFTVSMLVSIFTLAAMSVDRYVAIVHSRRSSSLRVSRNALLGVGF-IWALS 163
Shict:
        166 SLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEFFMSMFGKLYPL--LAFG--LPLFFASF 220
Query:
              + P + + H + + C P
                                              + KY+
                                                          FG LPL
Sbict:
        164 IAMASPVAYHQRLFHRDSNQTFCWEQWPN-----KLHKKAYVVCTFVFGYLLPLLLICF 217
Query:
        221 YFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLLSIAIISAVLWLPEWVAWLWVWHLKAAG 280
             + + + K+ K + +++ K+ +L + ++ + WLP V LW
Sbict:
        218 CYAKVLNHLHKK-LKNMSKKSEASKKKTAQTVLVVVVVFGISWLPHHVVHLWAEF--GAF 274
Query:
        281 PAPPOGET--ALSOVI MESISSANPI TELVMSEEFREGI KGVWKWMTTKKPPTVSESOF 337
                      + L +S SS NP+I+ +SE FR+ K V+K + + P SE++E
        275 PLTPASFFFRITAHCLAYSNSSVNPI IYAFLSENFRKAYKOVFKCHVCDESPR-SETKE 332
Sbict:
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# >sp:NY2R\_BOVIN-NEUROPEPTIDE Y RECEPTOR TYPE 2 (NPY2-R). Length = 384

Score = 153 bits (383), Expect = 5e-37

Identities = 93/308 (30%), Positives = 164/308 (53%), Gaps = 7/308 (2%)

Query: 47 DEDEDVTNSRTFFAAKIVIGMALVGIMLVCGIGNFIFIAALVRYKKLRNLTNLLIANLAI 106

D + ++ +S ++V+ +A I+L+ IGN + I ++++K +R +TN IANLA+
Sbict: 38 DSEPELIDSTKLIEVOVVLILAYCSITLIGVIGNSLVIHVVIKEKSMRTVTNEFIANIAV 97

Query: 107 SDFLVAIVCCPFEMDYYVVRQLSWEHGHVLCTSVNYLRTVSLYVSTNALLAIAIDRYLAI 166

+D LV +C PF + Y ++ + W+ G VLC V Y + +++ VST L IA+DR+ I
Sbict: 98 ADLLVNTLCLPFTLTYTLMGE--WKMGPVLCHLVPYAQGLAVQVSTITLTVIALDRHRCI 155

Querv: 167 VHPLRPRMKCQTATGLIALVWTVSILIAIPSAYFTTETVLVIVKSQEKIFCGQIWPVDQQ 226

V+ L ++ Q + +I L W VS L+A P A F +++ I+ E + C + WP +++
Sbict: 156 VYHLESKISKQISFLIIGLAWGVSALLASPLAIFREYSLIEIIPDFFIVACTFKWPGFFK 215

Querv: 227 -LYYKSYFLFIFGIEFVGPVVTMTLCYARISRELWFKAVPGFQTEQIRKRLRCRRKTVLV 285

+Y Y L I +V P+ ++ Y RI +L PG + +R R+KT +

Sbjct: 216 GIYGTIYSLSSLLILYVLPLGIISFSYTRIWSKLKNHVSPGAAHDHYHQR---RQKTTKM 272

Query: 286 LMCILTAYYLCWAPFYGFTIVRDFFPTVFVKEKHYLTAFYIVECIAMSNSMINTLCFVTV 345 L+C++ + + W P + F + D V + K Y F + IAM ++ N L + +

Sbjct: 273 LVCVVVVFAVSWLPLHAFQLAVDIDSHV-LDLKEYKLIFTVFHIIAMCSTFANPLLYGWM 331

Query: 346 KNDTVKYF 353

Sbjct: 332 NSNYRKAF 339

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>sp/P97926/OXYR MOUSE OXYTOCIN RECEPTOR (OT-R).
           Length = 388
 Score = 164 (57.7 bits), Expect = 8.9e-22. Sum P(2) = 8.9e-22
 Identities = 57/166 (34%). Positives = 84/166 (50%)
          24 WGLNLTLGOGAP-----ASGPPSR-----RVRLVFLGVILVVAVAGNTTVLCRLCGGG 71
Query:
            W+LLGGP
                                +GPP R
                                           RV + | +1| +A++GN VI |
          9 WSIELDLGSGVPPGAEGNLTAGPPRRNEALARVEVAVLCLILFLALSGNACVLLAL---- 64
Sbict:
Query:
          72 GPWAGPKRRKMDFLLVQLALADLYACGGTALSQLAWELLGEPRAATGDLACRFLQLLQAS 131
                  K ++ F + L++ADL
                                        L QL W++
                                                   R
                                                          DL CR ++ LQ
         65 -RTTRHKHSRLFFFMKHLSTADLVVAVFOVLPOLLWDTTF--RFYGPDLLCRLVKYLOVV 121
Shict:
Query:
         132 GRGASAHLVVLIALERRRAVRLPHGRPLPARA--LAALG-WLLALLLALPPAFV 182
            G AS +L++L++L+R A+ P. R L R LA L WL L+ ++P
Sbict:
         122 GMFASTYLLLLMSLDRCLAICOPL-RSLRRRTDRLAVLATWLGCLVASVPOVHI 174
 Score = 155 (54.6 bits), Expect = 8.9e-22, Sum P(2) = 8.9e-22
 Identities = 49/161 (30%). Positives = 85/161 (52%)
Query:
        217 CHGIFAPLPRWHLQVYAFYEAVAGFVAPVTVLGVACGHLLS--VWW--RHRPQAPAAAAP 272
            C +F + W + Y + +A ++ PV VL AC L+S +W R + A AAAA
Sbict:
         187 CWAVF--IQPWGPKAYVTWITLAVYIVPVIVLA-ACYGLISFKIWONLRLKTAAAAAAAE 243
Query:
        273 WSASPG-----RAPAPSALPRAKVQSLKMSLLLALLFVGCELPYFAARLAAAWS-SG 323
             S + G
                         R + + + AK++++KM+ ++ L F+ C P+F ++ + W +
        244 GSDAAGGAGRAALARVSSVKLISKAKIRTVKMTFIIVLAFIVCWTPFFFVQMWSVWDVNA 303
Sbict:
Query:
        324 PAGDWEGEGLSAALRVVAMANSALNPFVYLFFQAGDCRLRRQLRKRLGSLCCA 376
                        A+ ++A NS NP++Y+ F
                                                L +L +R LCC+
                F
Sbict:
        304 PK---EASAFIIAM-LLASLNSCCNPWIYMLFTG---HLFHELVQRF--LCCS 347
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>spl091178|GPRX ORYLA PROBABLE G PROTEIN-COUPLED RECEPTOR (FRAGMENT)
           Length = 428
 Score = 823 (289.7 bits), Expect = 9.8e-83, P = 9.8e-83
 Identities = 182/422 (43%), Positives = 266/422 (63%)
          2 ESSPIPQSSGNSSTLGRVPQTPGPSTASGVPEVGL----RDVASESVALFFMLLLDLTAV 57
Query:
            ++SP+ S + S
                                 P P+
                                        P+VG+ + + 1F M+ I+I A+
          5 KTSPMLTSDHSTSNESTGLEGPHPTVP----PDVGVVTSSQSQMKDLEGLECMVTLNLTAL 61
Shict:
Query:
          58 AGNAAVMAVIAKTPALRKFVFVFHLCLVDLLAALTLMPLAMLSSSALFDHALFGEVACRL 117
              N VM IA+ P L+KF FV HLC VD+L A+ LMPL ++SSS F +F + C++
Sbict:
          62 LANTGVMVATARAPHI KKEAEVCHI CAVDVI CATLI MPLGTTSSSPEEGTVVETTI ECOV 121
        118 YLFLSVCFVSLAILSVSAINVERYYYVVHPMRYEVRMTLGLVASVLVGVWVKALAMASVP 177
Query:
            Y+FL+V + L+IL+++AI+VERY+Y+VHPMRYEV+MT+ LV V++ +W K+L +A V
        122 YIFLNVFLIWLSILTITAISVERYFYIVHPMRYEVKMTINLVIGVMLLIWFKSLLLALVT 181
Sbjct:
        178 VLGRVSWEEGAPSVPPGCSLQWSHSAYCQLFVVVFAVLYFLLPLLLILVVYCSMFRVARV 237
Query:
                            CSL SHS
            +6 + +
                                        +F V+F V+ FL P+++I VY ++++VAR
        182 LFGWPPYGHOSSIAASHCSLHASHSRLRGVFAVLFCVICFLAPVVVIFSVYSAVYKVARS 241
Shict:
Query:
        238 AAMOHGP-LPTWME-TP-RORSESI SSRSTMVTSSGAPOT-TPHRTEGGGKAAVVI I AVG 293
            AA+Q P +PTW + +P + RS+S++S++T++T+ PQ +P R F GGKAA+ L +
        242 AALQQVPAVPTWADASPAKDRSDSINSQTTIITTRTLPQRLSPERAFSGGKAALTLAFIV 301
Sbict:
Query:
        294 GQFLLCWLPYFSFHLYVALSAQPISTGQVESVVTWIGYFCFTSNPFFYGCLNRQIRGELS 353
            GQFL+CWLP+F FHL ++L+ S G +E V W+ Y F NP FYG LNRQIR EL
Sbict:
        302 GOFLVCWLPFFIFHLOMSLTGSMKSPGDLEEAVNWLAYSSFAVNPSFYGLLNRQIRDELV 361
Query:
        354 K-OFVCFFKPAPEEELRLPSRFGSTEENFLOFLOGTGCPSFSWVSRPLPSPKO-EPPAVD 411
            K + C +P E+ S EGS +ENFLQF+Q T
                                                  SE+ S
                                                             +P+ E A
Shict:
        362 KFRRCCVTQPV---EIGPSSLEGSFQFNFLQFLQRTSSSSFTHPSFANSNPRNMFNQA-- 416
        412 FRIPGQIAEE 421
Query:
             +IPGQI EE
Sbjct:
        417 HKIPGQIPEE 426
```

>sp   P23	>sp P23749 RTA_RAT PROBABLE G PROTEIN-COUPLED RECEPTOR RTA.				
	Length = 343				
Score =	461 (162.3 bits), Expect = 2.3e-44, P = 2.3e-44 ies = 121/323 (37%), Positives = 178/323 (55%)				
Query:	2 NQTLNSSGTVESALNYSRGS-TVHT-AYLVLSSLAMFTCLCGMAGNSMVIWLLGFR 55 NQ G E+ YSRG T+ A L V + + + CLCG+ GN +V+W GF	5			
Sbjct:	13 NONKMCPGMSEALELYSRGFLTIEQIATLPPPAVTNYIFLLLCLCGLVGNGLVLWFFGFS 72	2			
Query:	56 MHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVNT-TDKVHELMKRLMYFAYTVGLS 11 + R PF IY L+LA+AD ++LFS A L ++ D V +++ + G+S	4			
Sbjct:	73 IKRTPFSIYFLHLASADGIYLFSKAVIALLNMGTFLGSFPDYVRRVSRIVGLCTFFAGVS 13	32			
Query:	115 LLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNE 17 LL AIS +RC+SV+FP+W+ RP+ LSA VC LLW L L+ + + FC FL + +	2			
Sbjct:	133 LLPAISIERCVSVIFPMWYWRRRPKRLSAGVCALLWLLSFLVTSIHNYFCM-FLGHEASG 19	1			
Query:	173 DRCFRYDMYQAALIMGVLTPYMTLSSLTLFYWYRRSSQQWRRQPTRLFYYVLASYLVFLI 23 C +D+ L+ + P+M L L L + V +++ R++ +L VYLA V VFL+	32			
Sbjct:	192 TACLNMDISLGILLFFLFCPLMVLPCLALILHVECRARR-RQRSAKLNHVVLAIVSVFLV 25	0			
Query:	233 CSLPLSIYWFVLYWL-SLPPEMQVLCFSLSRLSSSVSSSANPVIYFLVGSRRSHRLPTRS 29 S+ L I WF L+W+ +P ++ L ++SSA P++YFL G +S RI	1			
Sbjct:	251 SSIYLGIDWF-LFWVFQIPAPFPEYVTDLCICINSSAKPIVYFLAGRDKSQRL-WEP 30	5			
Query:	292 LGTVLQQALREEPELEGGETPTVGTNEM 319 L V Q+ALR+ EP TP T EM				
Sbjct:	306 LRVVFQRALRDGAEPGDAASSTPNTVTMEM 335	- 1			

>sp|Q98907|P2Y3\_CHICK P2Y PURINOCEPTOR 3 (P2Y3) (NUCLEOSIDE DIPHOSPHATE RECEPTOR). Length = 328

Score = 452 (159.1 bits), Expect = 2.0e-43, P = 2.0e-43 Identities = 85/185 (45%), Positives = 116/185 (62%)

Query: 15 CQFSEKYKQVYLSLAYSIIFILGLPLNGTVLWHFWGQTKRWSCATTYLVNLMVADLLYVL 74
C F E++KQV L L YS++F+LGLPLN V+ W K + T Y++NL +ADLLYV

Sbjct: 13 CTFHEEFKQVLLPLVYSVVFLLGLPLNAVVIGQIWLARKALTRITIYMLNLAMADLLYVC 72

Query: 75 -LPFLIITYSLDDRWPFGELLCKLVHFLFYINLYGSILLLTCISVHQFLGVCHPLCSLPY 133 LP LI Y+ D WPFG+ CK V F FY NL+GSII LTCISV +++G+CHPL S

Sbjet: 73 SLPLLIYNYTQKDYWPFGDFTCKFVRFQFYTNLHGSILFLTCISVQRYMGICHPLASWHK 132

Query: 134 RT-RRHAWLGTSTTWALVVLQLLPTLAFSHTDYINGQMIWYDMTSQENFDRLFAYGIVLT 192 + ++ WL + W +V+ Q LPT F+ T ++ YD++ + F YGI LT

Sbjct: 133 KKGKKLTWLVCAAVWFIVIAQCLPTFVFASTGTQRNRTVCYDLSPPDRSTSYFPYGITLT 192

Query: 193 LSGFL 197 ++GFL Sbjct: 193 ITGFL 197

>sp10028241A1AA RABIT ALPHA-1A ADRENERGIC RECEPTOR (ALPHA 1A-ADRENOCEPTOR) (ALPHA-1C ADRENERGIC RECEPTOR).

Length = 466

Score = 295 (103.8 bits), Expect = 1.0e-31, Sum P(2) = 1.0e-31Identities = 66/215 (30%), Positives = 113/215 (52%)

Query: 8 STRESNSSHTCMPLSKMPISLAHGIIRSTVLVIFLAASFVGNIVLALVLORKPOLLQVTN 67 S+SS+ P + P++++ I+ + +GNI++ I +

L VT+ Sbict: 5 SGNASDSSNCTHPPA--PVNISKAILLGVILGGLILFGVLGNILVIISVACHRHLHSVTH 62

Query: 68 RFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVVSV 127

+I NL V DLL S V P+ + +W FC ++ L AS+ ++ V+S+ Shict: 63 YYIVNLAVADI LLTSTVI PESATEFII GYWAEGRVECNIWAAVDVI CCTASITSI CVIST 122

Query: 128 DRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWG 187

DRY+ + +PL YP+ +TQRRG I W +++ S PI+GW Q A D+ +C + Sbict: 123 DRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPLFGWRQPAPDDET-ICQI-N 179

Query: 188 ASPSYTILSVVSFIVIPLIVMIACYSVVFCAARRO 222 P Y + S + +PL +++A Y V+ A+R+ Sbict: 180 FEPGYVLFSALGSFYVPLTIILAMYCRVYVVAKRF 214

Score = 106 (37.3 bits), Expect = 1.0e-31, Sum P(2) = 1.0e-31

Identities = 23/75 (30%), Positives = 41/75 (54%)

396 KAAKVIFIIIFSYVLSLGPYCFLAVLAVWVDVFTQVPQWVITIIIWLFFLQCCIHPYVYG 455 Query:

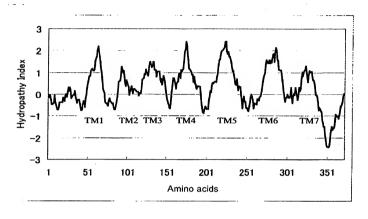
KAAK + I++ +VL P+ + + + + + P+ V I+ WL +L CI+P +Y

269 KAAKTLGIVVGCFVLCWLPFFLVMPIGSFFP-DFKPPETVFKIVFWLGYLNSCINPIIYP 327 Sbjct:

456 YMHKTIKKEIQDMLK 470 Query: + KK Q++LK Sbict: 328 CSSQEFKKAFQNVLK 342

10/34

Figure 10

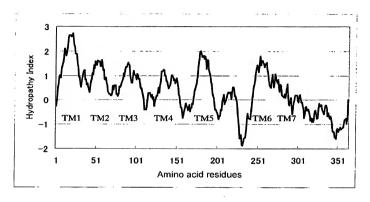


X64878	****** MEGALAANWSA-EAA-NASAAPPGAEGNRTAGPPRRNEALARVEVAYLCL
U82440	MEGELAANWST-EAV-NSSAAPPGAEGNCTAGPPRRNEALARYEVAVLCL
X93313	MEGLCLNLDCS-ELP-NSSWVNSSMENQNHSSNSTRDPLKRNEEVAKVEVTVLAL
X87783	MEEMFKEQDF-WSFNESSRNSTVGNETFGGNQTVNPLKRNEEVAKVEVTVLAL
AF184966	MEKPGNITLHPNGIDPFGRNEEVAGIEIMVLSI
X76321	MCD ANOTAG MCDPFGRNEEVAQIEIMVLSI
AF147743	MANUESERVOD STUDIES CONTROL OF THE STUDIES OF THE S
GPRv8	MKNFSFPMQD-STHQTESPPHRLLSLTNKSDPVGRPERDEQLAQVEIAVLGV
AE003754	MPANFTEGSFDSSGTGQTLDSSPVACTETVTFTEVVEGKEWGSFYYSFKTEQLITLWVI
MEUU3134	MKCDHTLFFALFQTEQFAVLWII
	TM1 ******** ******* TM2 *******
X64878	LLALSGNACVLLALRTTRQKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDITFRFYGP
U82440	FLALSGNACVLLALRITRHKHSRLFFFMKHLSIADLVVAVFQVLPQLLWDITFRFYGPI
X93313	LIVIZORUVCATTVEKI I KUKUZKELLEMKUTZI VNTAAVALÕATAÕTEMNI IEKELÕE
X87783	FLALAGNICVLLGIYINRHKHSRMYFFMKHLSIADLVVAIFQVLPQLIWDITFRFYAP
AF184966	FLALAGNLCVL I A I YTAKHTQSRMYYLMKHLS I ADL VVAVFQVLPQL I WD I TFRFYGPD
X76321	VVAVIGNVSVLLAMYNTKKKMSRMHLFIKHLSLADLVVAFFQVLPQLCWEITYRFFGPC
AF147743	FVAVIGNLSVLLAMHNTKKKSSRMHLFIKHLSLADMVVAFFQVLPQLCWEITFRFYGPD
AF14//43 GPRv8 ·	LTASVGNFILILVLWRRRKKLSRMYVFMLHLSIADLVVAFFQVLPQLIWDITDVFIGPD
	VFT1VGNSVVLFSTWR-RKKKSRMTFFVTQLAITDSFTGLVNILTDINWRFTGDFTAPD
AE003754	TVIVLGNSAVLFVMFINKNRKSRMNYFIKQLALADLCVGLLNVLTDIIWRITISWRAGA
	** ::: :: **: :::*:::*::*.:: * :* : : :
	0********* TM3 ********* TM4
K64878	LCRLVKYLQVVGMFASTYLLLLMSLDRCLAICQPLRSLRRRTDRLAVLATWLGCLVA
J82440	LCRŁYKYLQVVGMFASTYLLLLMSLDRCLAICQPLRSLRRRTDRLAVLATWLGCLVA
(93313	VCRLVTYLQVVGMFASTYMLLLMSLDRCLAICQPLRSLHRRSDCVYVLFTWILSFLL
(87783	LCRLVKYLQTVGMFASTYMLVLMSIDRCIAICQPLRSLHKRKDRCYVIVSWALSLVF
\F184966	LCRIVKHLQVTGNFASTYMMVMMTLDRYIAICHPLKTLQQPTQRSYIMIVSTWNCSLVF
(76321	LCRIVKHLQVLGMFASTYMMVMMTLDRYIAICHPLKTLOOPTORAYIMIGSTWICSIII
F147743	LCRIIKYLQLLGMFASTYMIVVMTVDRYQAVCYPMVTFOKKRALWNIPICTSWSISLII
PRv8	VCRVVRYLQVVLLYASTYVLVSLSIDRYHAIVYPMKFLQGEKQ-ARVLIVIAWSLSFLF
E003754	ACKAIRFSQVCVTYSSTYVLVAMSIDRYDAITHPMNFSKSWKR-ARHLVAGAWLISALF
	*: : .
	**********
64878	APQVHIFSLREVADGVFDCWAVFIQPWGPKAYITWITLAVYIVPVIVLATCYGLI
182440	APQVHIFSLREVADGVFDCWAVFIQPWGPKAYITWITLAVYIVPVIVLAACYGII
93313	TPQTVIFSLTEVGNGVYDCRADFIQPWGPKAYITWITLAVYIIPVMILSVCYGII
87783	VPQVY1FSLREIGNGVYDCWGDFVQPWGAKAYITWISLTIYIIPVA1LGGCYGII
F184966	TPQYF1FSLSEVKNGSTVKDCWAHF1EPWGARAY1TW1TGG1FLVPVV1LVMCYGF1
76321	TPQYFIFSLSEIQNGSYVYDCWGHFIEPWGIRAYITWITVGIFLIPVILMICYGFI
F147743	LPQVFIFSKIEISPGIFECWAEFIQPWGPRAYVTWILVVIFFIPSTILITCQVKI
PRv8	IPTLIIFGKRTLSNG-EVQCWALWPDDSYWTP-YNTIVAFLYYFIPLTIISINYGIV
E003754	LPILVLYEEKLIQGHPQCWIELGSPIAWQVYMSLVSATLFAIPALIISACYAII

X64878	EKINONI DI KTANAMATADECA ACCECCIVAL ADVICCIVAL ICKANI DELININI DELININI DI CONTROLLE DI CONTROLL
U82440	FKIWQNLRLKTAAAAAAEAPEGAAAGDGGRVALARVSSVKLISKAKIRTVKMTFIIVLAF
X93313	FKIWQNLRLKTAAAAAAEAPEGAAAGDGGRMALARVSSVKLISKAKIRTVKMTFIIVLAF YKIWQNIRLKTVCESNLRLSTSRRATLSRVSSVRLISKAKIRTVKMTFIIVLAY
X87783	
AF184966	FKIWQNFKRKTKKDQCITLTTAASKANALARVSSVKLVSKAKITTVKMTFYIVLAY HTIWKNIKYKKRKTIPGAASKNGLIGKNSVSSVTTISRAKLRTVKMTFYIVLAY
X76321	
AF147743	HSIWKNIKCKTMRGTRNTKDGMIGKYSVSSYTIISRAKLRTVKMTLVIVLAY
GPRV8	KIIKRNIYYKKQNEYQYTNQKQVLPSRASSVNCISKAMIKTYKMTIYTYYAY RTIWIKSKTYETVISNCSDGKLCSSYNRGLISKAKIKAIKYSIIIIIAF
AE003754	KTIWAKCSIFYPTERACFGAAPARRASSRGIIPRAKYKTYKMTLTIVFVF
AL003134	
	* : :::::::::::::::::::::::::::::::::::
	**************************************
X64878	IVCWTPFFFVQMWSVWDANAPKEASAFIIVMLLASLNSCCNPWIYMLFTGHLFHEIV
U8244D	IVCWTPFFFVQMWSVWDANAPKEASAFIIVMLLASLNSCCNPWIYMLFTGHLFHELV
X93313	I VCWTPFFFVQMWSVWDPNPPKEASLFI I AMLLGSLNSCCNPWI YMLFTGHLFHDLI
X87783	IVCWTPFFFVQMWSAWDPEAPREAMPFIISMLLASLNSCCNPWIYMFFAGHLFHDLK
AF184966	IICWAPFFTVQMWSVWDENFQYADSENTAVTISALLASLNSCCNPWIYMIFSGHLLQDFM
X76321	IVCWAPFF I VONWSYWDENFSWDDSENAAVTL SALLASLNSCCNPW I YMLFSGHLLYDFI
AF147743	VLCWSPFFIAQLWSVWFPSGITEGSAFTIIMLLGNLNSCTNPWIYMYFCGHJPY
GPRv8	ICCWSPYFLFDILDNFNLLPDT-QERFYASVIIQNLPALNSAINPLIYCVFSSSISFP
AE003754	IICWSPYIIFDLLQVFGQIPHS-QTNIAIATFIQSLAPLNSAANPLIYCLFSSQVFRTLS
	: **:*:: :: . : : * ***, ** ** * : :
X64878	QRFLCCSASYLKGRRLGETSASKKSNSSSFVLSHRSSSQRSCSQPS
U82440	QRFLCCSASYLKGNRLGETSTSKKSNSSSFVLSHRSSSQRSCSQPS
X93313	QSFLCCSARYLKTQQQGS-DLSASRKSNSSTFVLSRKSSSQKSITQPS
X87783	QSLLCCSTLYLKSSQCRCDQEHDSRKSNCSTYVIKSTSS-QRSITQSS
AF184966	NCFAWCRRANADFKKEDSDSSIRRTTLLTKMTN-RSPTGSTGNWRD
X76321	RCFPCCKKPRNMLQKEDSDSSTRRTTLLTKLAAGRMTNDGFGSWRD
AF147743	CTNKQLENTSAQEDSVVTGSIHLVD-RDPEENSTCA
GPRv8	CREQRSQDSRMTFRERTERHEMQILSKP-EF
AE003754	REPPEKWETCCCKSYRNNSQQNRCHTVGRRLHNSCDSMRTLTTSLTVSRRSTNKTNARVV
X64878	TA
U82440	TA
X93313	TA
X87783	17
AF184966	LDNSPKTSIQNE
X76321	PCNSRKSSQS IGLDCFCKSSQCLEHDCSRKSSQC   PLDCSRKSSQC   PLDCSRKSSQC   N
AF147743	
GPRv8	
AE003754	ICERPTKYVTVPAMSERRGVSLKGNTDIL
VC 4070	
X64878	<del></del>
U82440 X93313	
X87783	
AF184966	
X76321	KES
AF147743	VE9
GPRV8	
AE003754	
AE003134	

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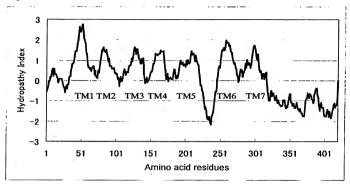
Figure 13



	\$\$\$\$\$\$\$\$\$\$\$ TM1 \$\$\$\$\$\$\$\$\$\$ \$\$\$\$\$\$\$\$\$ TM2 \$\$\$
GPRv12_ORF	MGPGEALLAGLLYMYLAYALLSNALYLLCCAYSAELRTRASGYLLYNLSLGHLLLAALDN
AF208288	MNSWDAGLAGLLVGT I GVSLLSNGLVLLCLLHSAD I RRQAPALFTLNLTCGNLLCTVVNN
	# :# ###### .:.#:####.##### :##::# :#:: :##: #:## :.::#
	******* Gessesses TM3 secesses
GPRv12_ORF	PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP
AF208288	PLTLAGVVAQRQPAGDRLCRLAAFLDTFLAANSMLSMAALSIDRWVAYVFPLSYRAKMRL
	*:** **:
	******** TM4 ******** @ ********
GPRv12_ORF	RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
AF208288	RDAAFMVAYTWLHALTFPATALALSWLGFHQLYASCTLCSRRPDERLRFAVFTSAFHALS
	* *.:::. :* ::*::.::*. ****:: , :***:*
	TM5 ********** **
GPRv12_ORF	FVLPLAVLCLTSLQVHRVARRHCQRMDTVTMKALALLADLHPSVRQRCLIQQKRRRHRAT
AF208288	FLLSFIVLCFTYLKVLKVARFHCKRIDVITMQTLVLLVDIHPSVRERCLEEQKRRRQRAT
	*:*.: ***:* *:* :** *:*:*:*::*::*,:**::*,:*:*:**::*** :*** :****::***
	###### TM6 #############################
GPRv12_ORF	RKIGIAIATELICEAPYVMTRLAELVPEVTVNAQWGILSKCLTYSKAVADPETYSLLRRP
AF208288	KKISTFIGTFLVCFAPYVITRLVELFSTAPIDSHWGVLSKCLAYSKAASDPFVYSLLRHQ
	[##, #,###;#####;###,##,;;;;##;####;##
CODula ODE	FROM ACHINER LYCTOPLICTURES BUILDINGS
GPRv12_ORF	FRQVLAGMVHRLLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
AF208288	YRRSCKELLNRIFNRRSIHSVGLTGDSHSQNILPVSE
	[#1 ][[#1]] # #, ,# , ][[# ]
GPRv12 ORF	QTH
AF208288	

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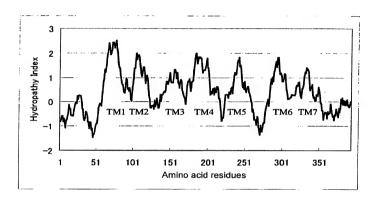




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}						######	
1	MLAAAFADSN	SSSMNVSFAH	LHFAGGYLPS	DSQDWRTIIP	ALLVAVCLV	G FVGNLCVIGI	60
	********	********	********	*******	*******	*********	;
	**	****	TM2 ##	***			
61	LLHNAWKGKP	SMIHSLILNL	SLADLSLLLF	SAPIRATAYS	KSVWDLGWF	/ CKSSDWF1HT	120
	********	****		*****	*******	::::::::::::::::::::::::::::::::::::::	:
	<b>@####</b> TM3	********		****	TM4 ###	******	
121	CMAAKSLTIV						
	*******	********	*********	********	*******	*********	
1	•	***	#### TM5	*******	****		
181	HEGVENCLVD	VPAVAEEFMS	MFGKLYPLLA	FGLPLFFASF	YFWRAYDQC	KRGTKTQNLR	240
	********	********	********	********	********	********	
	***	****** TI	M6 #####	****	****	**** TM7 **	
241	NQIRSKQVTV	MLLSIAIISA	VLWLPEWVAW	LWVWHLKAAG	PAPPQGFIAL	SQVLMFSISS	300
	*****						
	*******						
301	ANPLIFLYMS	EEFREGLKGV	WKWMITKKPP	TVSESQETPA	GNSEGLPDKV	PSPESPASIP	360
361	EKEKPSSPSS	GKGKTEKAEI	PILPDVEQFW	HERDTVPSVQ	DNDP I PWEHE	DQETGEGVK	419

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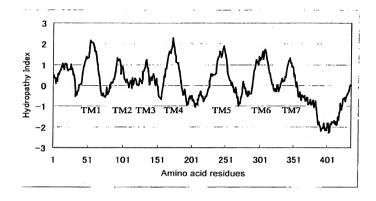
Figure 17



GPRv21	METTMGFMDDNATNTSTSFLSVLNPHGAHA-TSFPFN
AL121755	
AF236082	
U42766	MGP   GAEADENQTVEENKVEQYGP
U76254	MGPIGAEADENQTVEENKVEQYGP
U42389	MGPIGAEADENQTVEENKVEQYGP
U50144	MKMGPLGAEADENQTVEEMKVDQFGPG
D86238	MVLKMGPVGAEADEN-QTVEVKVEPYGPG
M81490	milivuddamreggaidegitietoty2FliuilYFLVDDEG2U1G1G211-1F2GF0
AF037444	MSMANSENSTSLFG KRHADVTGPHSASHDV DPSNTSVYYDHASNYESVLSTTSTLM
	######## TM1
GPRv21	FSYSDYDMPLDEDEDVINSRTFFAAKIVIGMALVGIMLVCGIGNFIF
AL121755	YGDYDLPMDEDEDMTKTRTFFAAKIVIGIALAGIMLVCGIGNFVF
AF236082	FSYGDYDMPLDEEEDVTNSRTFFAAK!VIGMALVGIMLVCGIGNFIF
U42766	QTTPRGELVPDPEPELIDSTKLIEVQVVLILAYCSIILLGVIGNSLV
U76254	QTTPRGELVPDPEPELIDSTKLIEVQVVLILAYCSIILLGVIGNSLV
U42389	QTTPRGELVPDPEPELIDSTKLIEVQVVLILAYCSIILLGVIGNSLV
U50144	HTTLPGELAPDSEPELIDSTKLIEVQVVLILAYCSIILLGVIGNSIV
D86238	HTTPRGELPPDPEPELIDSTKLVEVQVILILAYCSIILLGVVGNSLV
M81490	FETYNITYMMNFSCDDYDLLSEDMWSSAYFKIIVYMLYIPIFIFALIGNGTV
AF037444	LKLTDLVTPFNASEPDPESNGSDTDGGHAAISEQPMYAKVIIVLMYVLIILVAVGGNLLF
	# : . ::::: #::. ## .
GPRv21	####### ###### TM2 #####################
AL121755	AALVRYKKLRNLTNLL   ANLA   SDFLVA   VCCPFEMDYYVVRQLSWEHGHVLCTSVNYL
AF236082	AALTRYKKLRNLTNLL  ANLA  SDFLVA    CCPFEMDYYVVRQLSWEHGHVLCASVNYL
U42766	ITALARYKKLRNLTNLLIANLAISDFLVAIVCCPFEMDYYVVRQLSWEHGHVLCASVNYL
U76254	IHVVIKEKSMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHLVPYA
U42389	IHVVIKEKSMRTYTNEFIANLAVADLLVNTLCLPETLTYTLMGEWKMGPVLCHLVPYA
U50144	IHVVIKEKSMRTVTNEFIANLAVADLLVNTLCLPETLTYTLMGEWKMGPVLCHLVPYA
D86238	IHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHLVPYA IHVVIKFKSMRTVTNFFIANLAVADLLVNTLCLPFTLTYTLMGEWKMGPVLCHLVPYA
M81490	CYIVYSTPRMRTVTNYFIASLAIGDILMSFFCEPSSFISLFILN-YMPFGLALCHFVNYS
AF037444	CTITATOLEMENTALINE LIMITATED TANANT CHIRACTER AND THE AMBRECATE OF THE CHEANAS
WL021444	SYVIVMYPKMRSVTNLFLLNLAISDIVKAVICNPFAFIANLILL-YWPYGEFMCQVVTYI : :*.:** :: .**: .*
	## TM3 ########## ######################
GPRv21	RTVSLYVSTNALLAIAIDRYLAIVHPLRPRMKCQTATGLIALVWTVSILIAIPSAYFTTE
AL121755	RTVSLYVSTNALLAIAIDRYLAIVHPLKPRMNYQTASFLIALVWWVSILIAIPSAYFATE
AF236082	RTVSLYVSTNALLAIAIDRYLAIVHPLRPRMKCQTAAGLIFLVWSVSILIAIPAAYFTTE
U42766	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAIFREY
U76254	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALIASPLAIFRFY
U42389	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLGWRISALLASPLAIFREY
U50144	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKQISFLIIGLAWGVSALLASPLAIFREY
U50144 D86238	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKQISFLIIGLAWGVSALLASPLAIFREY QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAIFREY
U50144 D86238 M81490	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKQISFLIIGLAWGVSALLASPLAIFREY QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAIFREY QAVSVLVSAYTLVAISIDRYIAIMWPLKPRITKRYATFIIACVWFIALATALPIPIVSGI
U50144 D86238	QGLAVQVSTITLTVIALDRHRCIVYHLESKISKQISFLIIGLAWGVSALLASPLAIFREY QGLAVQVSTITLTVIALDRHRCIVYHLESKISKRISFLIIGLAWGISALLASPLAIFREY

TYLVIVKSQEKIFCGQIWPVDQQ-LYYKSYFLFIFGIEFGVPVYMTLCYARISRELI AL121755 TVLFIVKSQEKIFCGQIWPVDQQ-LYYKSYFLFIFGSVFVCPVYMTLCYARISRELI AF236682 TVLVIVERQEKIFCGQIWPVDQQ-TYYRSYFLFIFGSVFVCPVYMTLCYARISRELI U42766 SLIEIIPDFEIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U76254 SLIEIIPDFEIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 SLIEIIPDFEIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 SLIEIIPDFEIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 SLIEIIPDFEIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 SLIEIIPDFEIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 TKQSNSTGLCLEHFENDHNRYIYSLSILLILYVLPLGIISFSYTRIWSKLI U50144 TKQSNSTGLCLEHFENDHNRYIYSLITILITYVLPLGIISFSYTRIWSKLI U50145 S####################################		0 ####################################
AL121755 ATVLFIVKSQ-EKIFCGQI MPVDQQ-LYYKSYFLFIFGVEYVCPVYAMITCYARISRELI H27366 LV42766 SLIEIIPDF-EIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U76254 LV42389 SLIEIIPDF-EIVACTEKWPGEEKSIYGTYYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 SLIEIIPDF-EIVACTEKWPGEEKSIYGTYSLSSLLILYVLPLGIISFSYTRIWSKLI U50144 SLIEIIPDF-EIVACTEKWPGEEKGIYGTYSLSSLLILYVLPLGIISFSYTRIWSKLI M81490 DIPMSPWHTKCEKYICREWWPGEEKGIYGTYSLSSLLILYVLPLGIISFSYTRIWSKLI AF037444 TKQSNSTGLCLEHFENDHNRYIYSIVIMMLQYFVPLAVITYTHTHIGYIVW  * :	GPRv21	
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U42766  U42766  U42766  U50144  U50144  U50144  U50144  SLIE IPDF—EIVACTEKWPGEEKS IYGTVYSLSSLLILYVLPLGI ISFSYTR IWSKLI U50144  U50144  SLIE IPDF—EIVACTEKWPGEEKS IYGTVYSLSSLLILYVLPLGI ISFSYTR IWSKLI U50144  SLIE IPDF—EIVACTEKWPGEEKS IYGTVYSLSSLLILYVLPLGI ISFSYTR IWSKLI U50144  SLIE IPDF—EIVACTEKWPGEEKS IYGTVYSLSSLLILYVLPLGI ISFSYTR IWSKLI U50144  TKQSNSTGL——CLEHFENDHN—RYIYSLSTLLILYVLPLGI ISFSYTR IWSKLI TKQSNSTGL——CLEHFENDHN—RYIYSL IV IMMLQYFVPLAVI IFTVAR IT IRV  *: *: *: *: *: :: ::  ***: **: *: :: ::  ***: *: *: *: :: ::  ***: **:		TATELLANDA ENTECCUTABADOO CANDENCIT NEUT ECNOBANAMATI DA VONCOCET
U76254		CITETIONS ELIVACTERMINCER CITACIONEL COLLINION DI CITACIONA DI CITA
USD144		STIETLED EINVELENMAGERZIAGIALZEZ STEITLAFLEGIIZLZALEMZKI
USD1144		STIETIANE EINDETERMAGEERSTAGIAATERSTEINAN SI STIETIANE SI SESTIMINE SET
D86238		
### ### ### ### ### ### ### ### ### ##		STIETTPDFETVACTERWPGEERGTYGTTYSLSSLLTLYVLPLGTTSFSYTRTWSKL
### TKQSNSTGL		STIETTPDFELANCIERMAGEEKSAAGIAA2F2 IFTITAAFAFEEKSAALUNSKF
# : : # : # : # :		DISMOSTRI CENTICKEMMESKSQETTTILSLFALQFVVPLGVLIFTYARITIRVI
### ### ### ### ### ### ### ### ### ##	AFU3/444	
GPRv21         FKAYPG-FQTEQIRKRLRCRRKTVLVLMCILTAYVLCWAPFYGETIVRDFFPTVFVEKKH           AL121755         FKAYPG-FQTEQIRKRLRCRRKTVLVLMCILTAYVLCWAPFYGETIVRDFFPTVFVKEKH           AF236082         FKAYPG-FQTEQIRKRLRCRRKTVLVLMCILTAYVLCWAPFYGETIVRDFFPTVFVKEKH           AF236082         FKAYPG-FQTEQIRKTVRCRRRTVLGLVCVLSAYVLCWAPFYGETIVRDFFPSVFVKEKH           AVEYPG-FQTEQIRKTVRCRRRTVLGLVCVLSAYVLCWAPFYGETIVRDFFPSVFVKEKH         ANIVSPG-AANDHYHQRRQKTTKMLVCVVVVFAVSWLPLHAFQLAVD-IDSQVLDLKE           U42388         HNYSPG-AANDHYHQRRQKTTKMLVCVVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE           D86238         NHYSPG-AANDHYHQRRQKTTKMLVCVVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE           D86238         NHYSPG-AASHYHQRRQKTTKMLVCVVVVFAVSWLPLHAFQLAVD-IDSHVLDLKE           M81490         AKRPGCEATHROQRMASKRRLWKWMLTVVIVFTCCWLPFNILQLLLMDEEFAHWD           AF037444         IKKTPGCEAECROPGRMAASKRRLWKWMLTVVIVFTCWLPFNILQLLWDEFAHWD           XF1         XF1           CPRV21         YLTAFYIVECIAMSNSININTLCFVTVKNDTWKYFKKIML		
AL121755	CPPu21	
AF235082 FKAYPG-FQTEQIRRTYRCRRTYU.GU.VCVLSAYYU.GWAPFYGTIVRDFPSYVEKEK.  U76254 SYPSG-AANDHYHQRRQKTTKML.VCVVYVFASSW.PLHAFQLAVD-IDSQVLDLK.  U76254 SYPSG-AANDHYHQRRQKTTKML.VCVVYVFASSW.PLHAFQLAVD-IDSQVLDLK.  U42388 NHYSPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSQVLDLK.  U50144 NHYSPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  U81490 AKRPG-AASDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  WWASPG-AANDHYHQRRQKTTKML.VCVVVVFAYSWL.PLHAFQLAVD-IDSVLDLK.  ###################################		EXAMPLE FOREOUR PRODUCTION OF THE PRODUCT OF THE PR
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U42389		CHASEC WHITHINGS - BOXILLAND ACARAMALWASHIN MACATAMA - BOSSA DA MA
USD144		PHASEC-VANDUARIOS-BOKATANI ACAMANI VICANI DI TALCA YAR INDUSTRIA
D86238		MHASLG-WAUDHLUGKKGKIIKMI ACAAAALWASMILHIMEDI WAD IDGAMIDI KE
M81490		MHAZLO-VUUDULUKKKKKILKMITACAAAALVA2MILKITUVLAAAD IDSHAFDEKE
AF037444  IKKTPGEAEEDRDRRMAASKRRLVKMIII VYVIYAVCWLPYHVITLVGD-HNPDIYNQPH  ***  S\$		WINDLE VERNOUND WOCK DEMAKRIM TAN TALLOM DENT OF THE OLD FIRM DE
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CPRv21		
AL121755  VLTAFYVYECI AMSNSHINTVCFVTVKNHTMKYFKKMMLLHWRPSQRGSKA  V42766  VKLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFRCEQRLDAI HSEV  U76254  VKLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFRCEQRLDAI HSEV  U42388  VKLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFRCEQRLDAI HSEV  U50144  VKLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFRCEQRLDAI HSEV  U50144  VKLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFRCEQRLDAI HSEV  D86238  WSLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFRCEQRLDAI HSEV  D86238  VKLIFTVFHI IAMCSTFANPLLYGWMNSNYRKAFLSAFR	CDD21	******** TM7 ********
AF235082  V1.TAFYYVEC IAMSNSN INTLCFVTVRNNTSKYLKR I LR		TETATTI VECTAMONOMINITECTATANNI VAKTEKKIMEEHWKASYNGGKS
U42766		ALTACAMACTAMONOMINIACEATANNINKAEKKNINGFHMKb2dkC2K2
U76254		TETACHTIAMCCTCANDLA ACMINICHANA TORTE CACO
U42388		THE TELEVITAMEST FAMILY AGMINISTRACT CARE
USD144		THE ITEM AND STEAMENT AND
D86238		THE I FINE I I AMES I FANDE I AGMINISTRANCE DA PER CONTROL DE LA PROPERTICION DE LA PROPE
### ### ##############################		TAT TELIALULI VWC 2 LAWATT CRAWA 2 M. KWALT 2 VEDCERKTD VIH 2 FA
AF037444 MNVVWLCAQWLAMSHSCYNPFVYFSLSATFRRNLRRMTHACRLKQKR-LRQHLSMRSSRA :		TECHNICATION AND TECHNICATION AND TECHNICATION OF THE STATE OF THE STA
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AL 121755 S	AFUSTANA	
AL 121755 S	GPRv21	
AF236082 S — ADLDLRTTGI — PATEEYDCIRLK — U42766 SVTFKAK — KNLEVRKNSC — PNDSFTEATNV — U42868 SVTFKAK — KNLEVRKNSC — PNDSFTEATNV — U42389 SVTFKAK — KNLEVRKNSC — PNDSFTEATNV — U50144 SVTFKAK — KNLEVRKNSC — PNDSFTEATNV — U50144 SVTFKAK — KNLEVKNNC — PNDSFTEATNV — U50144 SVTFKAK — KNLEVKNNC — PNDSFTEATNV — U50144 SVTFKAK — KNLEVKNNC — PNDSFEATNV — U50147 —		SADI DI PTNCVDTTECVDCI DI V
U42766         SYTFKAKKNLEVRKNSGPNDSFTEATHV		SADI DI PTTCI PATECVDCI DI V
U76254 SVTFKAKKNLEVRKNSGPNDSFTEATNV		
U42389 SYTFKAKKNLEYRKNSGPNDSFTEATNY		
USD144 SYTEKAKKHLQYTKNNGPNDSFTETTNY		CALEKYKKNI EADKNCCDNUCETCYTANA
D86238 SMTFKAKKNLEVKKNNGPTDSFSEATNY		CALEKTKKAI UALKANG DADGELELIAA
M81490 SGTGPALPLNRMNTSTTYISARRKPRATSLRANPLSCGETSPLR		CMIERAK
		SCTCDAL DI NDMATCTTY I CARRYDDATCI DANDI COCCTORI D
NUMBER OF STREET		
		PUMPUPIET LOOKES IL SKASKOSTUSSUKOVKUAN I 220EMÕÕTKEKKTEGAZNDMAT

Figure 20



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1	MEDLFSPSIL	PPAPNISVPI	LLGWGLNLTL	GQGAPASGPP	SRRVRLVFLG	VILVVAVAGN	60
	********	********	********	********	********	*******	
	****		******	B TM2 B	*******		
61	TTVLCRLCGG	GGPWAGPKRR	KMDFLLVQLA	LADLYACGGT	ALSQLAWELL	GEPRAATGDL	120
	**********	*********	********	******	*******	********	
	A	TM3 sees			******	TM4 2222	
121	ACREL OLL DA	SCOCASAHI V	VI IAI EDDDA	VDI DUCDDI D	ARALAALGWL	LALLIALDDA	100
	VOIL FAFFAU	SUNUASAIIL	VEINEERRAN	VKEFFIGKFEF	ANALAALUWL	LALLLALFFA	100
					****	********	
	***						
						****** TM5	
181	FVVRGDSPSP	LPPPPPPTSL	QPGAPPAARA	WPGQRRCHGI	FAPLPRWHLQ	VYAFYEAVAG	240
	********				*********		
			*********	**********	*********		
_	*********					*****	
241	FVAPVTVLGV	ACGHLLSVWW	RHRPQAPAAA	APWSASPGRA	PAPSALPRAK	VQSLKMSLLL	300
	********	********	********	********	*********	**	
	# TM6 #####	****		******	TM7 #####	****	
301			CCCDACDWEC		AMANSALNPF		200
301	ALLI VOCELE	IT AARLAAAW	SSUFAGDWEG	EULSAALKIV	AMANJALNEE	ALLLEAVENC	300
361	RLRROLRKRL	GSL CCAPOGG	AFDFFGPRGH	OAL YRORWPH	PHYHHARREP	I DECCI REPE	42N
			······	4	·····	EDEGGEN! I'I	720
421	PRPRPLPCSC	ESAF					
	21 000						i

22/34

Figure 22

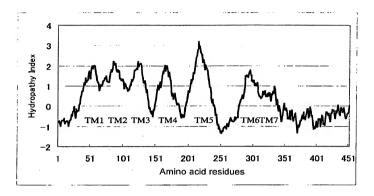


Figure 23

HSH2R 1	
D49783	
M32701	
U25440	
\$57565	
\$73473	
M74716	
U64032	MTFRDLLSVTFEGPRPD1SAGGSGAGGGAGAGAGAGDTASSESPAVGGVPGAAGGGGGG
L41147	
GPRv47	
D43633	
ucuan 1	
HSH2R_1 D49783	MAPNGTASSFCLDSTACKITIT
M32701	
	WISNGTGSSFCLDSPPCRIT
U25440	TYPSFCMDFTYYKVTIS
S57565	TVHSCCLDSMALKVTIS
S73473	MAPWPHKNGSLAFWSDAPTLDPSAANTSGLPG-VPW-AAA
M74716	MAPWPHKNGSLAFWSDAPTLDPSAANTSGLPG-VPW-AAA
U64032	VVGAGSGEDNRSSAGEPGGAGGGGEVNGTAAVGGLVVSAQSVGVG
L41147	MVPEPGPTANSTPAWGAGPPSAPGGSGWVA
GPRv47	MESSPIPQSSGNSSTLGRVPQTPGPSTASGVPEVGLRDV-ASESVAL
D43633	MMADKTSPMITSDHSISNFSTGLFGPHPTVPPDVGVVTSSQSQMKDLFGL
	ess TW1 sessess TM2 sesse
HSH2R_1	VLAVLILITVAGNYVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSC
049783	VLAVLILITVAGNVVVCLAVGLNRRLRNLTNCFIVSLAITDLLLGLLVLPFSAIYQLSC
N32701	VLTVL L T AGNVVVCLAVGLNRRLRSLTNCF VSLA TDLLLGLLVLPFSAFYQLSC
J25440	ILIILILYTVAGNYVYCLAVGLNRRLRSLTNCFIVSLAVTDLLLGLLVLPFSAIYQLSC
557565	VLTTLILITIAGNVVVCLAVSLNRRLRSLTNCFIVSLAATDLLLGLLVLPFSAIYQLSF
573473	AGALLALATYGGNLLVITAIARTPRLQTITNVFVTSLATADLVVGLLVMPPGATLALTG
174716	AGALLALATYGGNLLVITAIARTPRLQTITHYFYTSLATADLYYGLLYMPPGATLALTG
J64032	FLAAFILTAVAGNLLVILSVACNRHLQTVTNYFIVNLAVADLLLSATVLPFSATMEVLG
41147	ALCVVIALTAAANSLLIALICTQPALRNTSNFFLVSLFTSDLMVGLVVMPPAMLNALYG
PRV47	FMLLLDLTAVAGNAAVMAVIAKTPALRKEVEVEHLCLVDLLAALTLMPLAMLSSSALED
43633	CMVTLNLIALLANTGVMVAIARAPHLKKFAFVCHLCAVDVLCAILLMPLGIISSSPFFG
	ess Gennesses TM3 nessens m
ISH2R_1	WSFGKVFCNIYTSLDVMLCTASILNLFMISLDRYCAVMDPLRYPVLVTPARVAISLVLI
49783	WSFGKVFCN IYTSLDVMLCTAS I LNLFM I SLDRYCAVMDPL RYPVLVTPVRVA I SLVL II
32701	WSFGKVFCN1YTSLDVMLCTAS1LNLFM1SLDRYCAVTDPLRYPVL1TPVRVAVSLVL1
125440	WSFSKYFCNIYTSLDVMLCTASILNLFMISLDRYCAVTDPLRYPYLITPARVAISLVFI
57565	WSFGHVFCNIYTSLDVMLCTASILNLFMISLDRYCAVTDPLRYPVLVTPVRVAISLVFI
73473	WPLGATGCELWTSVDVLCVTASIETLCALAVDRYLAVTNPLRYGTLVTKRRARAAVVLV
74716	WPLGATGCELWTSVDVLCVTASIETLCALAVDRYLAVTNPLRYGTLVTKRRARAVVLVI
64032	WAFGRAFCDYWAAYDVLCCTASILSLCTISYDRYYGYRHSLKYPAIMTERKAAAILALLI
41147	WVLARGLCLLWTAFDVMCCSASILNLCLISLDRYLLILSPLRYKLRMTPLRALALVLGAI
PRv47	ALFGEVACRLYLFLSVCFVSLAILSVSAINVERYYYVVHPWRYEVRWTLGLVASVLVGVI
43633	VYFTILECQVYIFLNVFLIWLSILTITAISVERYFYIVHPMRYEVKMTINLVIGVMLLII
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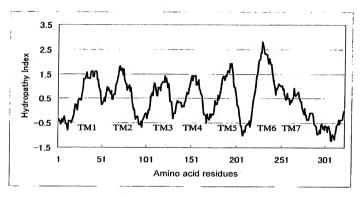
Figure 24

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HSH2R_1	VISITLSFLSIHLGWNSRNETSKGNHTTSKCNVQVNEVYGLVDGLVTFYLPLLIMCI
D49783	VISITLSFLSIHLGWNSRNETSKGNHTTSKCKVQVNEVYGLVDGLVTFYLPLLIMCI
M32701	VISITLSFLSIHLGWNSRNETSSFNHTIPKCKVQVNLVYGLVDGLVTFYLPLLVMCI
U25440	VISITLSFLSIHLGWNSRNETSKONDTIVKCKVQVNEVYGLVDGLVTFYLPLLIMCI
\$57565	VISITLSFLSIHLGWNSRNGTRGGN-DTFKCKVQVNEVYGLVDGLVTFYLPLLIMCV
S73473	IVSATVSFAPIMSQWWRVGADAEAQECHSNPRCCSFASNMPYALLSSSVSFYLPLLVMLF
M74716	VSATVSFAPIMSQWWRVGADAEAQECHSNPRCCSFASNMPYALLSSSVSFYLPLLVMLF
U64032	AVALVVS-MGPLLGMKEPVPPDERFCGITEEVGYAVFSSLCSFYLPMAVIVV
L41147	SLAALASFLPLLLGWHELGHARPPVPGQCRLLASLPFVLVASGLTFFLPSGAICF
GPRv47	VKALAMASVPVLGRVS-WEEGAPSVPPGCSLQWSHSAYCQLFVVVFAVLYFLLPLLLILV
D43633	FKSLLLA-LYTLFGWPPYGHQSSIAASHCSLHASHSRLRGVFAVLFCVICFLAPVVVIFS
	* 1 in * * 1
	t
HSH2R_1	TYYRIFRVARDQAKRID-HISSWKAATIR
D49783	TYYRIFKVARDQAKRIN-HISSWKAATIR
M32701	TYYRIFKIARDQAKRIH-HMGSWKAATIG
U25440	TYFRIFKIAREQARRIN-HIGSWKAATIR
\$57565	TYYRIFKIAREQAKRIN-HISSWKAATIR
S73473	VYARVFVVAKRQRRLLRRELGRFPPEESPRSPSRSPSPATVGTPTASDGVPSCGR
M74716	VYARVFVVAKRQRRFVRRELGRFPPEESPRSPSRSPSPATVGTPTASDGVPSCGR
U64032	MYCRVYVVARSTTRSLEAGVKRERGKASEVVLRIHCRGAASGADGAPGTRGAKGHTFRSS
L41147	TYCRILLAARKQAVQVASLTTGMASQASETLQVPRTPRPGVESADS
GPRv47	VYCSMFRVARVAAMQHGPLPTWMETPRQRSESLSSRSTMVTSSGA
D43633	VYSAVYKVARSAALQQVPAVPTWADASPAKDRSDSINSQTTIITTRTLP
	<b>*</b> : <b>*</b> : *
	******** TMG ****** *******
HSH2R_1	EHRATVTLAAVMGAFIICWFPYFTAFVYRGLRGDDAINEMLEAIYLWLGY
D49783	EHKATVTLAAVMGAFIICWFPYFTAFVYRGLRGDDAINEVLEAIVLWLGY
M32701	EHKATVTLAAVMGAFIICWFPYFTVFVYRGLKGDDAINEAFEAVVLWLGY
U25440	EHKATVTLAAVMGAFIICWFPYFTVFVYRGLKGDDAVNEVFEDVYLWLGY
\$57565	EHKATVTLAAVMGAFIICWFPYFTAFVYRGLRGDDAINEAVEGIVLWLGY
\$73473	RPARLLPLG-EHRALRTLGLIMGIFSLCWLPFFLANVLRALVGPSLVPSGVFIALNWLGY
M74716	RPARLLPLG-EHRALRTLGLIMGIFSLCWLPFFLANVLRALVGPSLVPSGVFIALNWLGY
U64032	LSVRLLKFSREKKAAKTLAIVVGVFVLCWFPFFFVLPLGSLFPQLKPSEGVFKVIFWLGY
L41147	RRLATKHSRKALKASLTLGILLGMFFYTWLPFFYANIYQAYC.—DCISPGLFDYLTWLGY
GPRv47	PQTTPHRTFGGGKAAVVLLAVGGQFLLCWLPYFSFHLYVALSAQPISTGQVESVVTWIGY
D43633	QRLSPERAFSGGKAALTLAFIYGQFLYCWLPFFIFHLQWSLTGSMKSPGDLEEAVNWLAY
	[# .# : # # : #:#:# .: . : #:.#
	TW7 #########
HSH2R 1	ANSALNPILYAALNRDFRTGYQQLFCCRLANRMSHKTSLRSNASQLSRTQSREPRQ
D49783	ANSALNPILYAALNRDFRTGYQQLFCCRLANRNSHKTSLRSNASQLSRTQSREPRQ
M32701	ANSAL NPI LYATL NRDFRTAYQQLFRCRPASHNAQETSLRSNSSQLARNQSREPMR
U25440	ANSALMPILYAALMRDFRTAYHQLFCCRLASHMSHETSLRLMMSQLMRSQCQEPRW
\$57565	ANSALNPILYAALNRDFRTAYQQLFHCKFASHNSHKTSLRLNNSLLPRSQSREGRW
S73473	VARACEMENT ACE CODE DE L'ALAGEMENTE DE L'ACE DE
M74716	ANSAFNPLIYCR-SPOFRDAFRILL-CSYGGRGPEEPRVVTFPASPVASR
U64032	ANSAFNPLIYCR-SPDFRDAFRRLL-CSYGGRGPEEPRVVTFPASPVASR
UB4U32 L41147	FNSCVNPLIYPCSSREFKRAFLRLLRCQCRRRRRRRPLWRYYGHHWRASAGGGPHPDCAL
GPRv47	CNSTMNP11YPLFMRDFKRALGRFLPCPRCPRERQAS-LASPSLRTSHSGPRPGLSL
D43633	FCFTSNPFFYGCLNRQIRGELSKQFVCFFKPAPEEELRLPSREGSIEENFLQF SSFAVNPSFYGLLNRQIRDELVKFRRCCVTQPVEIGPSSLEGSFQENFLQF
033	
	** :

HSH2R_1	QEEKPLKLQYWSGTEVT
D49783	QEEKPLKLQVWSGTEVTAPQGATDR
M32701	QEEKPLKLQVWSGTEVTAPRGATDR
U25440	QEDKPLNLQVWSGTEVTAPQGATNR
\$57565	QEEKPLKLQYWSGTELTHPQGNP1R
S73473	QNS-PLNRFDGYEGERP-FPT
M74716	QNS-PLNRFDGYEGERP-FPT
U64032	SAGAALPGAALALTAAPAPSSAAAPEGQAAGAGRRKPPCAFREWRLLGPLRRPTTOLRAK
L41147	QQVLPLPLPPDSDSDSDAGSGGSSGLRLTAQLLLPGEATQDPPLPTRAAAAVNFFNIDPA
GPRv47	LQGTGCPSESWVSRPLPSPKQEPPAVDFRIPGQIAEETSEFLEQQLTSDIIMSDSYLRPA
D43633	I QRTSSSSETHPSFANSNP-RNMENQAHK I PGQ I PEEQA
HSH2R_1	
D49783	
M32701	
U25440	
S57565	
S73473	
M74716	
U64032	VSSLSHK1RAGGAQRAEAACALRSEVEAVALSVARDVAEDNTCQAYELADYRNLRETD1
L41147	EPELRPHPLGIPTN
GPRv47	ASPRLES
D43633	

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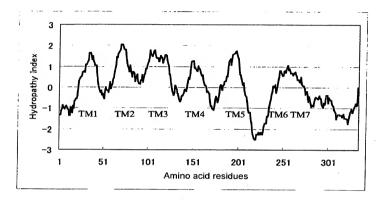




	********* TW1 *
GPRv51	MNQTLNSSGTVESALNYSRGSTVHTAYLVLSSLAMFTCLCGMA
M35297	MAGNCSWEAHSTNQNKMCPGMSEALELYSRGFLT!EQ!ATLPPPAVTNY!FLLLCLCGLV
	*** *: **** ,
	###### ####### TM2 ########
GPRv51	GNSMVIWLLGFRMHRNPFCIYILNLAAADLLFLFSMASTLSLETQPLVN-TTDKVHELMK
M35297	GNGLVLWFFGFSIKRTPFSIYFLHLASADGIYLFSKAVIALLNMGTFLGSFPDYVRRVSR
	**.:*:*::::::::::::::::::::::::::::::::
	SESSESS TM3 SESSESSES SESSESSES TM4 SESSESSES
GPRv51	RLMYFAYTVGLSLLTAISTQRCLSVLFPIWFKCHRPRHLSAWVCGLLWTLCLLMNGLTSS
M35297	VGLCTFFAGVSLLPA   S   ERCVSV   FPMWYWRRRPKRLSAGVCALLWLLSFLVTS   HNY
	: ::::*:************:**:**:**:*::::::::
	\$ SERBERSE THS BREERES
GPRv51	FCSKFLKFNE-DRCFRVDMVQAALIMGVLTPVMTLSSLTLFVWVRRSSQQWRRQPTRLFV
M35297	FCMFLGHEASGTACLNMDISLGILLFFLFCPLMVLPCLALILHVECRARRRQRS-AKLNH
	** 1: . *:.:*: . *:::: *:*::: *::::: *. ::::::::
	SERESEE THE SERESEES SERESEES THE SERESEES
GPRv51	VVLASVLVFLICSLPLSIYWFVLYWLSLPPEMQVLCFSLSRLSSSVSSSAMPVIYFLVGS
M35297	VVLAIVSVFLVSSIYLGIDWFLFWVFQIPAPFPEYVTDLCICINSSAKPIVYFLAGR
	**** * ***: *: *. * **::: :.:* : : :: *. ::. **::*::***.*
GPRv51	RRSHRLPTRSLGTVLQQALREEPELEGGETPTVGTNEMGA
M35297 -	DKSQRLWEP-LRVVFQRALRDGAEPGDAASSTPNTVTMEMQCPSGNAS
	:#:## # .#:#:###: ####. # ## .

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Figure 28



Y14705	######## TM1 ## mtsaesllftslgpspssgdgdcrfneefkfillpmsyavyfylglal
AJ277752	MTSADSLLFTSLGPSPSSGDGDCKFNEEFKFTLLPMSYAVVFVLGLAL
AF031897	MDAPYRMFSLAPWTPTPPWLGGNTTAAAEAKCYFNEEFKFILLPISYGIVFYYGLPL
X99953	MTED I MATSYPTFLTTPYLPMKLLMNLTNDTED I CVFDEGFKFILLPYSYSAVFMVGLPL
AF069555	MSMANFTAGRNSCTFQEEFKQVLLPLVYSVVFLLGLPL
X98283	MSMANFTGGRNSCTFHEEFKQVLLPLVYSVVFLLGLPL
D63665	MERDNGTIQAPGLPPTTCYYREDFKRLLLPPYYSYYLYVGLPL
GPRv71	EKYDMNTSQEQGLCQFSEKYKQYYLSLAYSIIFILGLPL
	* : * : * : * * * :::::***
Y14705	######################################
AJ277752	NAPTLWLFLFRLRPWDATATYMFHLALSDTLYYLSLPTLYYYYAARNHWPFGTGFCKFYR
AF031897	NSWAMW I FYSRWRPWNATTYWFNLAISDTLYYFSLPTLYYYYADRNNWPFGKYFCK I YR
X99953	NIAAMWIFIAKMRPWNPTTYYMFNLALSDTLYYLSLPTLYYYYADKNNWPFGEVLCKLYR
AF069555	NAVVIGQIWLARKALTRITIYMLNLATADLLYVCSLPLLIYNYTQKDYWPFGDFTCKFVR
X98283	NAVYIGQIWLARKALTRTTIYMLNLAMADLLYVCSLPLLIYNYTQKDYWPFGDFTCKFVR
D63665	NVCVIAQICASRRTLTRSAVYTLNLALADLLYACSLPLLIYNYARGDHWPFGDLACRLVR
GPRv71	NGTVLWHFWGQTKRWSCATTYLVNLMVADLLYVL-LPFL!!TYSLDDRWPFGELLCKLYH
	* .: : : :: * .:* :* ** *: *: : : **** *::*:
	••.
	SEETM3 SEESSESSESS SEESSESS TM4 SEESS
Y14705	FLFYWNLYCSVLFLTCISVHRYLGICHPLRAIRWGRPR-FASLICIGYWI VVACCI VPNI
AJ277752	FLFYWNLYCSVLFLTCISVHRYMGICHPLRAIRWGRPR-FAGLLCLGYWLYVAGCLVPNL
AF031897	FLFYANLYSSILFLTCISVHRYMGICHPIRSLKWVKTK-HARLICVGVWLVVTICI IPNI
X99953	FLFYANLYSSILFLTCISVHRYRGVCHPITSLRRMNAK-HAYVICALVWLSVTLCIVPNI
AF069555	FQFYTNLHGS1LFLTC1SVQRYMG1CHPLASWHKKKGKKLTWLVCAAYWF1V1AQCLPTF
X98283	FQFYTNLHGSILFLTCISYQRYMGICHPLAS#HKKKGKKLTWLVCAAVWFIVIAQCIPTF
063665	FLFYANLHGS   LFLTC   SFQRYLG   CHPLAPWHKRGGRRAAWVVCGVVW  VVTAQC  PTA
GPRv71	FLFYINLYGSILLLTCISVHQFLGVCHPLCSLPYRTRR-HAWLGTSTTWALVVLQLLPTI
	* ** **: *:*:******: . : : : .* * :*.
	## ####### TMS ######
14705	FFVTTNANGTTILCHDTTLPEEFDHYVYFSSAVMYLLFGLPFLITLVCYGI MARRI VRPI
13277752	FFVTTNANGTTILCHDTTLPEEFDHYVYFSSTIMVLLFGFPFLITLVCYGLMARRIYRPI
F031897	IFVTTSSKDNSTLCHDTTKPEEFDHYVHYSSSIMALLFGIPFLVIVVCYCLMAKRLCKRS
(99953	IFYTYSPKYKNTICHDTTRPEDFARYVEYSTAIMCLLFGIPCLIIAGCYGLMTRELMKPI
NF069555	VFASTGTQRNRTVCYDLSPPDRSASYFPYGITLTITGFLLPFAAILACYCSMARII COKD
K98283	VFASTGTQRNRTVCYDLSPPDRSTSYFPYGITLTITGFLLPFAAILACYCSMARILCQKD
063665	VFAATGI-QRNRTVCYDLSPPILSTRYLPYGMALTVIGFLLPFTALLACYCRMARRLCRQD
GPRv71	AFSHTDY INGQMIWYDMTSQENFDRLFAYGIVLTLSGFLSLLGHFGVLFTDGQEPDQARG
	* * : : : : : : : : : : : : : : : : : :
	sessess TMG sessesses as
14705	PGAGQSSSRLRSLRTIAVVLTVFAVCFVPFHITRTIYYQAR-LLQADCHYLNIVNVV
J277752	PGAGQSSSRLRSLRTIAVVLTVFAVCFVPFHITRTIYYLAR-LLNAECRVLNIVNVV
F031897	FPSPSPRVPSYKKRSIKMIIIVETVFAICFVPFHITRTLYYTSR-YFQADCQTLNIINFT
99953	VSGNQQTLPSYKKRSIKTIIFVMIAFAICFMPFHITRTLYYYAR-LLGIKCYALNVINYT
F069555	ELIGLAVH-KKKDKAVRMIIIVVIVFSISFFPFHLTKTIYLIVRSSPTLPCPTLQAFAIA
98283	ELIGLAVH-KKKDKAVRMIIIVVIVFSISFFPFHLTKTIYLIVRSSASLPCPTLQAFAIA
63665	GPAGPYAQ-ERRSKAARMAYYYAAVFVISFLPFHITKTAYLAVRSTPGVSCPVLETFAAA
PRv71	EPHEDRQHSPSQVHPDHPTGVWPLHPLFCALPYHSLLLPHHLLSAFSGLPALDGSQCGLQ

	##### TM7 ########
Y14705	YKYTRPLASANSCLDPVLYLFTGDKYRNQLQQLCRGSKPKPRTAASSL
AJ277752	YKYTRPLASANSCLDPVLYLFTGDKYRNQLQQLCRGSTPKRRTTASSL
AF031897	YKITRPLASINSCLDPILYFMAGDKYRGRLRRGAAQRP-RPVPTSL
X99953	YKYTRPLASANSCIDPILYFLANDRYRRRLIRTYRRRSSVPNRRCMHTNHPQTEPHMTAG
AF069555	YKCTRPFASMNSVLDPILFYFTQRKFRESTRYLLDKMSSKWRHD
X98283	YKCTRPFASMNSVLDPILFYFTQRKFRESTRYLLDKMSSKWRDD
D63665	YKGTRPFASANSVLDPILFYFTQQKFRRQPHDLLQKLTAKWORD
GPRv71	DMEASGECEQLPQPSPVLSFKGGKNRVRLLQKLRQNKLGEHPAGRK
	:
Y14705	ALVTLHEESISRWADTHQDSTFSAYEGDRL
AJ277752	ALYTLHEESISRWADIHQDSIFPAYEGDRL
AF031897	LALVSPSVDSSVVGSCCNSESRGMGTVWSRGGQ
X99953	PLPV I SAEE I PSNGSMYRDENGEGSREHRVEWTDTKE I NQMMNRRST I KRNSTDKNDMKE
AF069555	HCITYGS
X98283	HC SYGS
D63665	RV
GPRv71	RCPGLNRSG
Y14705 AJ277752 AF031897 X99953 AF069555	NRHGENYLPYVEVVEKEDYETKRENRKTTEQSSKTNAEQDELQTQIDSRLKRGKWQLSSK
X98283	
D63665	
GPRv71	
Y14705	
AJ277752	
AF031897	
X99953	KGAAQENEKGHMEPSFEGEGTSTWNLLTPKMYGKKDRLAKNVEEVGYGKEKELQNFPKA
AF069555	
X98283	
D63665	
GPRv71	

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Figure 31

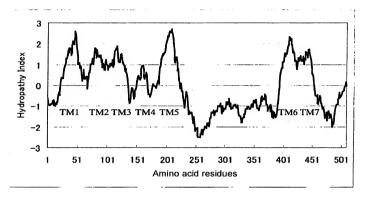


Figure 32

U03866
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D32202
D32201
APO13261  USYACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFEVLGYWAFGRVFCNI WAAVDV 1LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFEVLGYWAFGRVFCNI WAAVDV 1LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFEVLGYWAFGRVFCNI WAAVDV 1083261  ILSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 1083261  ILSVACHRILGVTHYY I VNLAVADLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 1083261  ILSVACHRILGVTHYYF I VNLAVADLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 10832202  ACCASI ILSVACHRILGVTHYYF I VNLAVADLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 1083261  UCCASI INGLI ISI IDRY I GVSYPLRYPT I VTQRGG MALLCVWALSLVI SI GPLFGWR-10832202  LCCTAS I MGCLI ISI I DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832201  LCCTAS I MGCLI ISI I DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832201  LCCTAS I I LSTALLT I SI DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832202  LCCTAS I I LSTALT I SI DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832202  LCCTAS I I BLGVI SI DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10
APO13261  USYACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFEVLGYWAFGRVFCNI WAAVDV 1LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFEVLGYWAFGRVFCNI WAAVDV 1LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFEVLGYWAFGRVFCNI WAAVDV 1083261  ILSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 1083261  ILSVACHRILGVTHYY I VNLAVADLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 1083261  ILSVACHRILGVTHYYF I VNLAVADLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 10832202  ACCASI ILSVACHRILGVTHYYF I VNLAVADLLTSTVLPFSA IFE ILGYWAFGRVFCNI WAAVDV 1083261  UCCASI INGLI ISI IDRY I GVSYPLRYPT I VTQRGG MALLCVWALSLVI SI GPLFGWR-10832202  LCCTAS I MGCLI ISI I DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832201  LCCTAS I MGCLI ISI I DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832201  LCCTAS I I LSTALLT I SI DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832202  LCCTAS I I LSTALT I SI DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10832202  LCCTAS I I BLGVI SI DRY I GVSYPLRYPT I VTQRRGG MALLCVWALSLVI SI GPLFGWR-10
U03126 S71323 WVPVLDMMTPSSVTL—MCSNCSHVLAPE——LATVKAVVLGUVLGIF ILFGVLGNLV AF091890 GPRV72  U03866 L31774 L31824 L31874 L31886 L31886 L31886 L31886 L31886 L31886 L318866 L
S71323 MVPVLDMMTPSSVTL—MCSNCSHVLAPE——LINTVKAVVLGWYLCIFILEGV IGNILV D63859
D63859 MTPSSVTLNCSNCSHVLAPELNTVKAVVLGMVLGIFILEGVIGNILV AF091890  GPRV72
GPRV72
GPRV72
U03866 LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV ILSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D32202 LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D32202 LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D32201 LSVACHRILHSVTHYY I VNLAVADLLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D4101201 LSVACHRILHSVTHYY I VNLAVADLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D4101201 LSVACHRILHSVTHYY I VNLAVADLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D411231 LSVACHRILHSVTHYY I VNLAVADLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D411231 LSVACHRILHSVTHYY I VNLAVADLLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D411231 LSVACHRILHSVTHYY I VNLAVADLLTSTVLPFS AI FEILGRWAFGRVFCN I WAAVDV D411231 LSVACHRILGVTYYF I VNLAVADLLTSTVLPFS AI FEILGRWAFGRVFCN I WAAVDV D411231 LSVACHRILGVTYYF I VNLAVADLLTSTVLPFS AI FEILGRWFGRVFCN I WAAVDV D411231 LSVACHRILGVTYYF I VNLAVADLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D411231 LSVACHRILGVTYYF I VNLAVADLTSTVLPFS AI FEVLGYWAFGRVFCN I WAAVDV D411231 LSVACHRILGVTYF I VNLAVADLTSTVLPF AI FEVLGYWAFGRVFCN I WAAVDV D411231 LSVACHRILGVTWAFGRVFCN I WAAVDV D411231 LSVAC
U03866 L31774 ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D25235 ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D25235 ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32201 ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV AF013261 ILSVACHRHHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV AF013261 ILSVACHRHHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV U07126 ILSVACHRHHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV U07126 ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGRWFGRVFCNI WAAVDV S71323 ILSVVCHRHLGTVTYYFI VNLAVADLLLTSTVLPFSAIFEILGRWFGRVFCNI WAAVDV S71323 ILSVVCHRHLGTVTYYFI VNLAVADLLLSSTVLPFSAIFEILGRWFGRVFCNI WAAVDV S71323 ILSVVCHRHLGTVTYYFI VNLAVADLLLSSTVLPFSAIFEILGRWFGRVFCNI WAAVDV S71324 ILSVCHRHLGTVTYYFI VNLAVADLLLSSTVLPFSAIFEILGRWFGRVFCNI WAAVDV AF091890 VVTLYKKSVLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGRVWCNNFSALLYL : * : : . : * : : * : : * . : * : : * . : * : : * . : * : : * : : * : : * : : * : : * : : * : : : * : : * : : * : : * : : * : : * : : * : : * : : : * : : * : : : * : : * : : : : * : : : * : : : * : : : * :
U03866 L31774 L31774 L31774 L31774 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D25235 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32202 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32201 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32201 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV U81982 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV U71126 LISVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV S71323 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGRWFGRVFCNI WAAVDV U71126 LISVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGRWFGRVFCNI WAAVDV U71126 LSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGRWFGRVFCNI WAAVDV VTLYKKSVLLTISNKFVFSTLTSNFLLSVLLVFFVVTSSIRREWI FGRVWFCNI WAAVDV VVTLYKKSVLLTISNKFVFSTLTSNFLLSVLLVFFVVTSISIRREWI FGRVWFCNSTALLYL CFRV72 ALVLQRKPQLLQVTNRFI FNLLVTDLLQI SLVAPWVVATSVPLFWPLNSHFCTALVSLTH  : : : : : : : : : : : : : : : : : : :
U03866 LISVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FEVLGYWAFGRVFCN! WAAVDV D25235 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FEVLGYWAFGRVFCN! WAAVDV D32202 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FEVLGYWAFGRVFCN! WAAVDV D32201 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FEVLGYWAFGRVFCN! WAAVDV D32201 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FEVLGYWAFGRVFCN! WAAVDV U81982 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FE!LGYWAFGRVFCN! WAAVDV U71126 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FE!LGYWAFGRVFCN! WAAVDV D7126 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FE!LGYWAFGRVFCN! WAAVDV D7126 JLSVACHRHLHSVTHYY! VNLAVADLLLTSTVLPFSA!FE!LGYWAFGRVFCN! WAAVDV D63859 JLSVACHRHLHSVTHYY! VNLAVADLLLSSTVLPFSA!FE!LGRWYFGRVFCN! WAAVDV VTLYKKSYLLTISSKFVFST.TLSNFLLSVLVLPFVVTSS!RREW!FGRVMFCN! WAAVDV VYTLYKKSYLLTISSKFVFST.TLSNFLLSVLVLPFVVTSS!RREW!FGRVMFSALLYL CFRV72 ALVLQRKPQLLQVTNRF!FNLLVTDLLQISLVAPWVVATSVPLFWPINSHFCTALVSLTH  ### ### ### ### ### ### ### ### ### #
L31774  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFGN WAAVDV D25235  LISVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFGN WAAVDV D32202  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFGN WAAVDV D32201  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFGN WAAVDV U81982  LISVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFGN WAAVDV U07126  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFGN WAAVDV U07126  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFGN WAAVDV U07126  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFGN WAAVDV U07127  LSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFGN WAAVDV WATLYKKYLLTLSNKFVFSLTLSNFLLSVTLPFSAIFEILGRWYFGRVFGN WAAVDV WYTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYL CFRV72  ALVLQRKPQLLQVTNRFIFHLLVTDLLQISLVAPWVVATSVLFWPHSHSHFCTALVSLTH  STM3 \$
D25235 D32202 D32201 D32202 D32202 D32201 D32202 D32201 DSVACHRILHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32202 D32201 DSVACHRILHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32361 DSVACHRILHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D31982 USVACHRILHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV D07126 DSVACHRILHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV D63859 LSVACHRILHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV D63859 LSVACHRILGYVTYYFI VNLAVADLLLSSTVLPFSAIFEILDRWVFGRVFCNI WAAVDV D63859 LSVACHRILGYVTYYFI VNLAVADLLLSSTVLPFSAIFEILDRWVFGRVFCNI WAAVDV AF091890 VVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYL  EXTRA S####################################
D32202  ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV D32201  ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV AF013261  ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV U81982  ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV U07126  ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV S71323  ILSVACHRHLHSVTHYYI VNLAVADLLLTSTVLPFSAIFEILGRWWFGRVFCNI WAAVDV AF091890  USVACHRHLGTVTYYFI VNLAVADLLLSSTVLPFSAIFEILGRWFGRVFCNI WAAVDV SFORD  VVTLYKKSYLLTISKKFVFSITLSNFLLSVLLSVLLPFVVTSSIRREWIFGVVWCNFSALLYL  STM3 \$
D32201  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV AF013261  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEVLGYWAFGRVFCNI WAAVDV U81982  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV U07126  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV S71323  ILSVACHRHLHGVTYYYFIVNLAVADLLLSSTVLPFSAIFEILGYWAFGRVFCNI WAAVDV AF091890  VVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFSAIFEILDRWYGRVFCNI WAAVDV AFVO91890  VVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVVWCNFSALLYL  STM3 \$
AF013261  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRYFCNI WAAVDV U81982  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRYFCNI WAAVDV U07126  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRYFCNI WAAVDV S71323  ILSVACHRHLHSVTHYYIVNLAVADLLLTSTVLPFSAIFEILGRWYFGRYFCNI WAAVDV HAF091890  VTLYKKSYLLTISNKFVFSTLISNFLUSVLISTSIRREWIFGRVMFSAILFIL GPRV72  ALVLQRKPQLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPTINSHFCTALVSLTH  :
AFO13261  USYACHRHLHSVTHYY1VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDV U07126  ILSVACHRHLHSVTHYY1VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDV ILSVACHRHLHSVTHYY1VNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDV S71323  ILSVACHRHLGYTYYFYIVNLAVADLLLTSTVLPFSAIFEILGYWAFGRVFCNIWAAVDV AFO91890  VVTLYKKSYLLTLSNKFVFSLTLSNFLLSVTVLPFSVAIFEILDRWYGRVFCNIWAAVDV AFVO91890  VVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFSVTSSIRREWIFGVYWCNFSALLYL  LCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWALSLVISIGPLFGWR- LCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWALSLVISIGPLFGWR- D252235  LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWALSLVISIGPLFGWR- D32200  LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWALSLVISIGPLFGWR- D32201  LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWALSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAMSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVISIGPLFGWR- LCCTASIMGCCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCWAWSLVYRGWIFGWR-
JUD1726  ILSVACHRILHSVTHYY1 VNIAVADILLISTVLPFSAIFEILCDRWAFGRVFCNI WAAADDV 571323  ILSVVCHRILGIVTYYFI VNIAVADILLISSTVLPFSAIFEILORWVFGRVFCNI WAAADDV AFO91890  GPRV72  ALVLQRKPQLLQVTNRFI FINLLVTDLLQI SLVAPWVVATSVPLFWHISHOTAL VSL LVLLQFVVATSVPLFWPLNSHFCTAL VSLTH  : : * :: * :: .: * :: .: * .: .: * .: .: * :  # TM3 ### S################################
JUD1726  ILSVACHRILHSVTHYY1 VNIAVADILLISTVLPFSAIFEILCDRWAFGRVFCNI WAAADDV 571323  ILSVVCHRILGIVTYYFI VNIAVADILLISSTVLPFSAIFEILORWVFGRVFCNI WAAADDV AFO91890  GPRV72  ALVLQRKPQLLQVTNRFI FINLLVTDLLQI SLVAPWVVATSVPLFWHISHOTAL VSL LVLLQFVVATSVPLFWPLNSHFCTAL VSLTH  : : * :: * :: .: * :: .: * .: .: * .: .: * :  # TM3 ### S################################
\$71323   ILSYVCHRHLQTVTYYF I VNLAVADLLLSSTVLPFSAIFEILDRWYGRVFCNI WAAVDV D63859   ILSYVCHRHLQTVTYYF I VNLAVADLLLSSTVLPFSAIFEILDRWYGRVFCNI WAAVDV AF091890   VVTLYKKSYLLTLSNKFVFSLTLSNFLLSVLVLPFVVTSSIRREWIFGVYWCNFSALLYL   LUSAND   L
D63859 AF091890 CPRV72 ALYLQKKSYLITLSNKFYSITLSNFLLSVLVLPFVVTSSIRREWIFGVWCMFSALLYL CPRV72 ALYLQKKPQLLQVTNRFIFNLLVTDLLQISLVAPWVVATSVPLFWPLNSHFCTALVSLTH  : : * :: : * :: : * :: * :: * :: * ::
AF091890  QPRV72  ALVLQRKPQLLQVTNRFIFNLLVTDLQISLVAPWVVATSVPLFWPLNSHCTALVSLTH  : : : * :: : * :: : * : : : : : * :
GPRV72  ALVLQRKPQLLQVTMRF FMLLVTDLLQISLVAPMVVATSVPLFWPLNSHFCTALVSLTH  :: + :: :: + :: : + :: : + :: : + : : : . : .
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U03866 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- L31774 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D25235 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32202 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32201 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- AF013261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR-
U03866 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- L31774 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D25235 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32202 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32201 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- AF013261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR-
LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D25235 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32202 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32201 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- AF013261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISIGPLFGWR-
LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D25235 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32202 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32201 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- AF013261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISIGPLFGWR-
DZSZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZZ
D32202 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- D32201 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- AF013261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTORRGLRALLCVWAFSIVISVGPIFGWR-
D32201 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- AF013261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPLFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTQRRGLRALLCVWAFSLVISVGPIFGWR-
AFUI3261 LCCTASIMGLCIISIDRYIGVSYPLRYPTIVTQRRGLMALLCVWALSLVISIGPEFGWR- U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTORRGLRALLCVWAFSLVISVGPIFGWR-
U81982 LCCTASIISLCVISIDRYIGVSYPLRYPTIVTORRGLRALLCVWAFSLVISVGPIFGWR-
U07126 LCCTASINGICIISIDRYIGVSYPIRYPTIVTORRCVPALLICVMVI SIVISICRI ECMP
S71323 LCCTASIMSLCVISVDRYIGVSYPLRYPAINTKRRALLAVMILWVLSVIJSIGPLEGWK-
D63859 LCCTASIMSLCVISVDRYIGVSYPLRYPAIMTKRRALLAVMLLWVLSVIISIGPLFGWK-
AF091890 LISSASMLTLGVIAIDRYYAVLYPMVYPMKITGNRAVMALVYIWLHSLIGCLPPLFGWSS
GPRV72 LFAFASVNTIVVVSVDRYLSIIHPLSYPSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGO
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	## 0 ######## TM5 #########
U03866	QPAPEDETICQINEEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKS
L31774	QPAPEDETICQINEEPGYVLFSALGSFYLPLAIILVMYCRYYVVAKRESRGLKS
D25235	QPAPEDETICQINEEPGYVLFSALGSFYLPLAIILVMYCRYYVVAKRESRGLKS
D32202	QPAPEDETICQINEEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKS
D32201	QPAPEDETICQINEEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKS
AF013261	QPAPEDETICQINEEPGYVLFSALGSFYLPLAIILVMYCRVYVVAKRESRGLKS
U81982	QPAPDDETICQINEEPGYVLFSALGSFYVPLTIILAMYCRYYVVAKRESRGLKS
U07126	QPAPEDETICQINEEPGYVLFSALGSFYVPLAIILVMYCRYYVVAKRESRGLKS
S71323	EPAPEDETYCKITEEPGYAIFSAYGSFYLPLAIILAMYCRYYVVAQKESRGLKE
D63859	EPAPEDETVCKITEEPGYAIFSAVGSFYLPLAIILAMYCRYYVVAQKESRGLKE
AF091890	VEFDEFKWMCVAAWHREPGYTAFWQIWCALFPFLVMLVCYGFIFRVARVKARKVHC
GPRy72	AAFDERNALCSMIWGASPSYTILSVVSFIVIPLIVMIACYSVVFCAARROHALLYNVKRH
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U03866	GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVG-
L31774	GLKTDKSDSEQVTLR1HRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLG1VVG-
D25235	GLKTDKSDSEQVTLR1HRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLG1VVG-
D32202	GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVG-
D32201	GLKTDKSDSEQVTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVG-
AF013261	GLKTDKSDSEQYTLRIHRKNAPAGGSGMASAKTKTHFSVRLLKFSREKKAAKTLGIVVG-
U81982	GLKTDKSDSEQVTLRIHRKNAPAGGSGVASAKNKTHFSVRLLKFSREKKAAKTLGIVVG-
U07126	GLKTDKSDSEQVTLRIHRKNVPAEGGGVSSAKNKTHFSVRLLKFSREKKAAKTLGIVVG-
\$71323	GQKIEKSDSEQVILRMHRGNTTVSEDEALRSRTHFALRLLKFSREKKAAKTLGIVVG-
D63859	GQKIEKSDSEQVILRMHRGNTTVSEDEALRSRTHFALRLLKFSREKKAAKTLGIVVG-
AF091890	GTYVI VEEDAQRTGRKNSSTSTSSSGSRRNAFQGYYYSANQCK-ALITILYVLG-
GPRv72	SLEVRYKDCVENEDEEGAEKKEEFQDESEFRRQHEGEVKAKEGRMEAKDGSLKAKEGS
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	####### TMG ############################
U03866	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
L31774	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
D25235	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
D32202	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
D32201	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
AF013261	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
U81982	CFVLCWLPFFLVMPIGSFFPDFKPPETVFKIVFWLGYLNSCIN
U07126	CFVLCWLPFFLVMPIGSFFPDFKPSETVFKIVFWLGYLNSCIN
S71323	CFVLCWLPFFLVLPIGSIFPAYRPSDTVFKITFWLGYFNSCIN
D63859	CFVLCWLPFFLVLPIGSIFPAYRPSDTVFKITFWLGYFNSCIN
AF091890	AFMYTWGPYMVVIASEALWGKSSVSPSLETWATWLSFASAVCH
GPRv72	TGTSESSVEARGSEEVRESSTVASDGSMEGKEGSTKVEENSMKADKGRTEVNQCSIDLGE
	* : : * ::

Figure 34

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U03866	-PITYPCSSQEFKKAFQNVLRTQCLCRKQSSKHALGYT-LHPPSQAVEGQHK
L31774	-PITYPCSSQEFKKAFONVI RIQCI RRKQSSKHAI CVT-I HPPSQAVECQUIV.
D25235	-PITYPCSSQEFKKAFQNVLRTQCLRRKQSSKHALGYT-LHPPSQAVEGQHK
D32202	-PITYPCSSQEFKKAFQNVLRTQCLRRKQSSKHALGYT-LHPPSQAVEGQHK
D32201	-PITYPCSSQEFKKAFQNVLRIQCLRRKQSSKHALGYT-LHPPSQAVEGQHK
AF013261	-PITYPCSSQEFKKAFQNVLRTQCLCRKQSSKHALGYT-LHPPSQAVEGQHK
U81982	-PITYPCSSQEFKKAFQNVLKTQCLRRKQSSKHALGYT-LHAPSQALEGQHK-
U07126	-PIIYPCSSQEFKKAFQNVLRIQCLRRRQSSKHALGYT-LHPPSQALEGQHR-
\$71323	TITIOS SECTION AND AND AND AND AND AND AND AND AND AN
D63859	-PITYLCSNQEFKKAFQSLLGVHCLRMTPRAHHHHLSVGQSQTQGHSLTISLDSK(
AF091890	-PITYLCSNQEFKKAFQSLLGVHCLRMTPRAHHHHLSVGQSQTQGHSLTTSLDSK(
	-PLIYGLWNKTVRKELLGMCFGDRYYREPFVQRQRTSRLFSISNR-
GPRv72	DDMEFGEDDINFSEDDVEAVNIPESLPPSRRNSNSNPPLPRCYQCKAAKVIFIIIFS
	:: . ::.
U03866	DMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARVRSKS
L31774	DMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARVRSKS
D25235	DWALL DAGRETE ALICATOR ACEMALL SOMEREZ WILL ASKDAZ SCITAKAKSK
D32202	DMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARVRSKS
D32201	DMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARTKSRS
AF013261	DMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARGHTPM
	DMVRIPVGSRETFYRISKTDGVCEWKFFSSMPRGSARITVSKDQSSCTTARRGMDC
U81982	DMVRIPVGSGETFYKISKTDGVCEWKFFSSMPRGSARITVPKDQSACTTARVRSKS
U07126	DMVRIPVGSGETFYKISKTDGVCEWKFFSSMPQGSARITVPKDQSACTTARVRSKS
S71323	APCRLSPSSSVALSRTPSSRDSREWRVFSGGPINSGPGPTEAGRAKVAKLCNKS
D63859	APCRLSPSSSVALSRTPSSRDSREWRVFSGGPINSGPCPTFAGPAKVAKI CHKS
AF091890	-ITDLGLSPHLTALMAGGOPLGHSSSTGDTGFSCSODSCN
GPRv72	YVLSLGPYCFLAVLAVWVDVETQVPQWVITIIIWLFFLQCCIHPYVYGYMHKTIKKEIQD
: :	
U03866	FLQVCCCVGPS-TPSLDKNHQVPTIKVHTISLSENGEEV
L31774	FLQVCCCVGPS-TPSLDKNHQVPT1KVHT1SLSENGEEV
D25235	FLEVCCCVGPS-TPSLDKNHQVPTIKVHTISLSENGEEV
D32202	VTRLECSGMILAHCNLRLPGSRDSPASASQAAGTTGDVPPGRRHQAQI IEVELV
D32201	T
AF013261	RYFTKNCREHIKHVNFMMPPWRKGLEC
U81982	FLQVCCCVGPS-TPNPGEN-HQVPTIKIHTISLSENGEEV
U07126	FLQVCCCVGSS-APRPEENHQVPTIKIHTISLGENGEEV
\$71323	LHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSEKGESV
D63859	LHRTCCCILRARTPTQDPAPLGDLPTIKIHQLSLSEKGESV
AF091890	-LRAL
GPRv72	MLKKFFCKEKPPKEDSHPDLPGTEGGTEGKIVPSYDSATFP
	THE THE PARTY OF T
U03866	
L31774	
D25235	
D32202	ETGFHHVGQDDLDLLTS
D32201	
AF013261	
U81982	
U07126	
\$71323	
D63859 NF091890	